

ATGAGCTCCCGAATCGTCAGGGAGCTGCCTTAGTCGTACCCCTTCCTCCACTTGACCAGG
M S S R I V R E L A L V V T L L H L T R

GTGGGGCTCTCCACCTGCCCGCTGACTGCCACTGCCCCCTGGAGGCGCCCAAGTGGCGG
V G L S T C P A D C H C P L E A P K C A

CCGGGAGTCGGGCTGGTCCGGGACGGCTGGGGCTGTTGTAAGTCTGCGGCAAGCAGCTC
P G V G L V R D G C G C C K V C A K Q L

AACGAGGACTGCAGAAAAACGCGCCCTGCCACACACCAAGGGCTGGAATGCAACTTC
N E D C R K T Q P C D H T K G L E C N F

GGGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGCAGACCTGT
G A S S T A L K G I C R A Q S E G R P C

GAATATAACTCCAGAATCTACCAAAACGGGAAAGTTTCCAGGCCCAACTGTAAACATCAG
E Y N S R I Y Q N G E S F Q P N C K H Q

TGCACATGTATTGGATGGCGCGGGGGCTTGCAATTCCTCTGTGTCCTCCCAAGAACTATCT
C T C I G W R R G A C I P L C P Q E L S

CTCCCCAACTTGGGCTGTCCCAACCCCTGGCTGGTCAAGTTACCGGGCAGTGTGCGGAG
L P N L G C P N P R L V K V T G Q C C E

MATCH WITH FIG.1B

FIG.1A

MATCH WITH FIG.1A

GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

GGCAAGGGGCTGGGATTGCGATGCGCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G K G L G F D A S E V E L T R N N E L I

GCAGTTGGAAAAAGGCAGCTCAGTGAAGCGGCTCCCTGTTTTGGAAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCCTTTACAAGGCCAGAAATGTATTGTTCAAAACAATTTCATGGTCCCAGTGC
L Y N P L Q G G Q K C I V Q T T S W S Q C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTAAGAAACCCGGATTICTGAGGTGGGCTTGTGGACAGCCAGTGACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCCAGTCAGGTTTACT
L K K G K K C S K T K K S P E P V R F T

MATCH WITH FIG.1C

FIG.1B

MATCH WITH FIG. 2A

FIG. 2B

1 MSSRIVRELALVVTLLHL.TRVGLS.TCPADCHCPL.EAPKCAPGVGLVR 47
 1 MLASVAGPIISLALVLLALCTRPATGQDCSAQCQCAEAAPHCPAGVSLVL 50
 48 DGGCCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEG 97
 51 DGGCCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK.DG 99
 98 RPCEYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCP 147
 100 APCVFGGSVYRSGESFQSSCKYQCTCLD.GAVGCVPLCSMDVRLPSPDCP 148
 148 NPRLVKVTGQCCEEWVCEDESIKDPMEDQDGLLGKGLGFDASEVELTRNN 197
 149 FPRRVKLPKCKCKEWCDEPKDRTAV.....GPALAAAYRLEDT... 186
 198 ELIavgKGSsLKRLPVFGMEPRILYNPLQGQKCIvQTTSWSQCSKTCGTG 247
 187FGPDPTMM.....RANCLVQTTEWSACSCKTCGMG 215
 248 ISTRVTNDNPECLVKETRICEVRPCGQPVYSSLKKGKCKSKTKKSPEPV 297
 216 ISTRVTNDNTFCRLKQSRLCMVRPCEADLEENIKKGKCKIRTPKIAKPV 265
 298 RFTYAGCLSVKKTTRPKYCGSCVDGRCCCTPQLTRTVKMRFPCEdGETFSKN 347
 266 KFELSGCTSVKTTTAKFCGVCTDGRCCCTPHRTTTLpVEFKCPDGEIMKKN 315
 348 VMMIQSSKCNYNCPHANE..AafPFYRLFQ 375
 316 MMFIKTCACHYNCpGNDIfESLYYRKMYG 345

FIG.3